

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/714,470

Source: IFW

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# ***ENTERED***



IFWO

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/714,470

DATE: 11/09/2004

TIME: 16:39:52

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\11092004\J714470.raw

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3 <110> APPLICANT: DIETZ, HARRY C.
4   ARKING, DAN E.
6 <120> TITLE OF INVENTION: DETECTION OF A PREDISPOSITION FOR THE DEVELOPMENT OF
7   CORONARY ARTERY DISEASE
9 <130> FILE REFERENCE: 60277(71699)
11 <140> CURRENT APPLICATION NUMBER: 10/714,470
12 <141> CURRENT FILING DATE: 2003-11-13
14 <150> PRIOR APPLICATION NUMBER: 60/425,865
15 <151> PRIOR FILING DATE: 2002-11-13
17 <160> NUMBER OF SEQ ID NOS: 6
19 <170> SOFTWARE: PatentIn Ver. 3.2
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 549
23 <212> TYPE: PRT
24 <213> ORGANISM: Homo sapiens
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30 Leu Ser Leu Leu Leu Val Leu Leu Gly Leu Gly Gly Arg Arg Leu Arg
31           20           25           30
33 Ala Glu Pro Gly Asp Gly Ala Gln Thr Trp Ala Arg Phe Ser Arg Pro
34           35           40           45
36 Pro Ala Pro Glu Ala Ala Gly Leu Phe Gln Gly Thr Phe Pro Asp Gly
37           50           55           60
39 Phe Leu Trp Ala Val Gly Ser Ala Ala Tyr Gln Thr Glu Gly Gly Trp
40   65           70           75           80
42 Gln Gln His Gly Lys Gly Ala Ser Ile Trp Asp Thr Phe Thr His His
43           85           90           95
45 Pro Leu Ala Pro Pro Gly Asp Ser Arg Asn Ala Ser Leu Pro Leu Gly
46           100          105          110
48 Ala Pro Ser Pro Leu Gln Pro Ala Thr Gly Asp Val Ala Ser Asp Ser
49           115          120          125
51 Tyr Asn Asn Val Phe Arg Asp Thr Glu Ala Leu Arg Glu Leu Gly Val
52           130          135          140
54 Thr His Tyr Arg Phe Ser Ile Ser Trp Ala Arg Val Leu Pro Asn Gly
55   145          150          155          160
57 Ser Ala Gly Val Pro Asn Arg Glu Gly Leu Arg Tyr Tyr Arg Arg Leu
58           165          170          175
60 Leu Glu Arg Leu Arg Glu Leu Gly Val Gln Pro Val Val Thr Leu Tyr
61           180          185          190
63 His Trp Asp Leu Pro Gln Arg Leu Gln Asp Ala Tyr Gly Gly Trp Ala
64           195          200          205
66 Asn Arg Ala Leu Ala Asp His Phe Arg Asp Tyr Ala Glu Leu Cys Phe

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67      210      215      220
69 Arg His Phe Gly Gly Gln Val Lys Tyr Trp Ile Thr Ile Asp Asn Pro
70 225      230      235      240
72 Tyr Val Val Ala Trp His Gly Tyr Ala Thr Gly Arg Leu Ala Pro Gly
73      245      250      255
75 Ile Arg Gly Ser Pro Arg Leu Gly Tyr Leu Val Ala His Asn Leu Leu
76      260      265      270
78 Leu Ala His Ala Lys Val Trp His Leu Tyr Asn Thr Ser Phe Arg Pro
79      275      280      285
81 Thr Gln Gly Gly Gln Val Ser Ile Ala Leu Ser Ser His Trp Ile Asn
82      290      295      300
84 Pro Arg Arg Met Thr Asp His Ser Ile Lys Glu Cys Gln Lys Ser Leu
85 305      310      315      320
87 Asp Phe Val Leu Gly Trp Phe Ala Lys Pro Val Phe Ile Asp Gly Asp
88      325      330      335
90 Tyr Pro Glu Ser Met Lys Asn Asn Leu Ser Ser Ile Leu Pro Asp Phe
91      340      345      350
93 Thr Glu Ser Glu Lys Lys Phe Ile Lys Gly Thr Ala Asp Phe Phe Ala
94      355      360      365
96 Leu Cys Phe Gly Pro Thr Leu Ser Phe Gln Leu Leu Asp Pro His Met
97      370      375      380
99 Lys Phe Arg Gln Leu Glu Ser Pro Asn Leu Arg Gln Leu Leu Ser Trp
100 385      390      395      400
102 Ile Asp Leu Glu Phe Asn His Pro Gln Ile Phe Ile Val Glu Asn Gly
103      405      410      415
105 Trp Phe Val Ser Gly Thr Thr Lys Arg Asp Asp Ala Lys Tyr Met Tyr
106      420      425      430
108 Tyr Leu Lys Lys Phe Ile Met Glu Thr Leu Lys Ala Ile Lys Leu Asp
109      435      440      445
111 Gly Val Asp Val Ile Gly Tyr Thr Ala Trp Ser Leu Met Asp Gly Phe
112      450      455      460
114 Glu Trp His Arg Gly Tyr Ser Ile Arg Arg Gly Leu Phe Tyr Val Asp
115 465      470      475      480
117 Phe Leu Ser Gln Asp Lys Met Leu Leu Pro Lys Ser Ser Ala Leu Phe
118      485      490      495
120 Tyr Gln Lys Leu Ile Glu Lys Asn Gly Phe Pro Pro Leu Pro Glu Asn
121      500      505      510
123 Gln Pro Leu Glu Gly Thr Phe Pro Cys Asp Phe Ala Trp Gly Val Val
124      515      520      525
126 Asp Asn Tyr Ile Gln Val Ser Gln Leu Thr Lys Pro Ile Ser Ser Leu
127      530      535      540
129 Thr Lys Pro Tyr His
130 545
134 <210> SEQ ID NO: 2
135 <211> LENGTH: 1012
136 <212> TYPE: PRT
137 <213> ORGANISM: Homo sapiens
139 <400> SEQUENCE: 2
140 Met Pro Ala Ser Ala Pro Pro Arg Arg Pro Arg Pro Pro Pro Gln Ser

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141	1			5					10					15	
143	Leu	Ser	Leu	Leu	Val	Leu	Leu	Gly	Leu	Gly	Gly	Arg	Arg	Leu	Arg
144				20				25					30		
146	Ala	Glu	Pro	Gly	Asp	Gly	Ala	Gln	Thr	Trp	Ala	Arg	Phe	Ser	Arg
147			35					40					45		Pro
149	Pro	Ala	Pro	Glu	Ala	Ala	Gly	Leu	Phe	Gln	Gly	Thr	Phe	Pro	Asp
150		50					55				60				Gly
152	Phe	Leu	Trp	Ala	Val	Gly	Ser	Ala	Ala	Tyr	Gln	Thr	Glu	Gly	Trp
153	65					70				75					80
155	Gln	Gln	His	Gly	Lys	Gly	Ala	Ser	Ile	Trp	Asp	Thr	Phe	Thr	His
156					85					90					95
158	Pro	Leu	Ala	Pro	Pro	Gly	Asp	Ser	Arg	Asn	Ala	Ser	Leu	Pro	Leu
159			100						105					110	Gly
161	Ala	Pro	Ser	Pro	Leu	Gln	Pro	Ala	Thr	Gly	Asp	Val	Ala	Ser	Asp
162			115						120					125	Ser
164	Tyr	Asn	Asn	Val	Phe	Arg	Asp	Thr	Glu	Ala	Leu	Arg	Glu	Leu	Gly
165		130					135					140			Val
167	Thr	His	Tyr	Arg	Phe	Ser	Ile	Ser	Trp	Ala	Arg	Val	Leu	Pro	Asn
168	145					150					155				160
170	Ser	Ala	Gly	Val	Pro	Asn	Arg	Glu	Gly	Leu	Arg	Tyr	Tyr	Arg	Leu
171					165					170				175	
173	Leu	Glu	Arg	Leu	Arg	Glu	Leu	Gly	Val	Gln	Pro	Val	Val	Thr	Tyr
174				180					185					190	
176	His	Trp	Asp	Leu	Pro	Gln	Arg	Leu	Gln	Asp	Ala	Tyr	Gly	Gly	Trp
177			195					200					205		Ala
179	Asn	Arg	Ala	Leu	Ala	Asp	His	Phe	Arg	Asp	Tyr	Ala	Glu	Leu	Cys
180		210					215					220			Phe
182	Arg	His	Phe	Gly	Gly	Gln	Val	Lys	Tyr	Trp	Ile	Thr	Ile	Asp	Asn
183	225					230					235				240
185	Tyr	Val	Val	Ala	Trp	His	Gly	Tyr	Ala	Thr	Gly	Arg	Leu	Ala	Pro
186				245						250					255
188	Ile	Arg	Gly	Ser	Pro	Arg	Leu	Gly	Tyr	Leu	Val	Ala	His	Asn	Leu
189				260					265					270	Leu
191	Leu	Ala	His	Ala	Lys	Val	Trp	His	Leu	Tyr	Asn	Thr	Ser	Phe	Arg
192			275					280					285		Pro
194	Thr	Gln	Gly	Gly	Gln	Val	Ser	Ile	Ala	Leu	Ser	Ser	His	Trp	Ile
195		290					295					300			Asn
197	Pro	Arg	Arg	Met	Thr	Asp	His	Ser	Ile	Lys	Glu	Cys	Gln	Lys	Ser
198	305					310					315				Leu
200	Asp	Phe	Val	Leu	Gly	Trp	Phe	Ala	Lys	Pro	Val	Phe	Ile	Asp	Gly
201				325						330					335
203	Tyr	Pro	Glu	Ser	Met	Lys	Asn	Asn	Leu	Ser	Ser	Ile	Leu	Pro	Asp
204				340					345					350	Phe
206	Thr	Glu	Ser	Glu	Lys	Lys	Phe	Ile	Lys	Gly	Thr	Ala	Asp	Phe	Phe
207			355						360				365		Ala
209	Leu	Cys	Phe	Gly	Pro	Thr	Leu	Ser	Phe	Gln	Leu	Leu	Asp	Pro	His
210		370					375					380			Met
212	Lys	Phe	Arg	Gln	Leu	Glu	Ser	Pro	Asn	Leu	Arg	Gln	Leu	Leu	Ser
213	385					390					395				400

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215 Ile Asp Leu Glu Phe Asn His Pro Gln Ile Phe Ile Val Glu Asn Gly
216                               405                               410                               415
218 Trp Phe Val Ser Gly Thr Thr Lys Arg Asp Asp Ala Lys Tyr Met Tyr
219                               420                               425                               430
221 Tyr Leu Lys Lys Phe Ile Met Glu Thr Leu Lys Ala Ile Lys Leu Asp
222                               435                               440                               445
224 Gly Val Asp Val Ile Gly Tyr Thr Ala Trp Ser Leu Met Asp Gly Phe
225                               450                               455                               460
227 Glu Trp His Arg Gly Tyr Ser Ile Arg Arg Gly Leu Phe Tyr Val Asp
228 465                               470                               475                               480
230 Phe Leu Ser Gln Asp Lys Met Leu Leu Pro Lys Ser Ser Ala Leu Phe
231                               485                               490                               495
233 Tyr Gln Lys Leu Ile Glu Lys Asn Gly Phe Pro Pro Leu Pro Glu Asn
234                               500                               505                               510
236 Gln Pro Leu Glu Gly Thr Phe Pro Cys Asp Phe Ala Trp Gly Val Val
237                               515                               520                               525
239 Asp Asn Tyr Ile Gln Val Asp Thr Thr Leu Ser Gln Phe Thr Asp Leu
240                               530                               535                               540
242 Asn Val Tyr Leu Trp Asp Val His His Ser Lys Arg Leu Ile Lys Val
243 545                               550                               555                               560
245 Asp Gly Val Val Thr Lys Lys Arg Lys Ser Tyr Cys Val Asp Phe Ala
246                               565                               570                               575
248 Ala Ile Gln Pro Gln Ile Ala Leu Leu Gln Glu Met His Val Thr His
249                               580                               585                               590
251 Phe Arg Phe Ser Leu Asp Trp Ala Leu Ile Leu Pro Leu Gly Asn Gln
252                               595                               600                               605
254 Ser Gln Val Asn His Thr Ile Leu Gln Tyr Tyr Arg Cys Met Ala Ser
255                               610                               615                               620
257 Glu Leu Val Arg Val Asn Ile Thr Pro Val Val Ala Leu Trp Gln Pro
258 625                               630                               635                               640
260 Met Ala Pro Asn Gln Gly Leu Pro Arg Leu Leu Ala Arg Gln Gly Ala
261                               645                               650                               655
263 Trp Glu Asn Pro Tyr Thr Ala Leu Ala Phe Ala Glu Tyr Ala Arg Leu
264                               660                               665                               670
266 Cys Phe Gln Glu Leu Gly His His Val Lys Leu Trp Ile Thr Met Asn
267                               675                               680                               685
269 Glu Pro Tyr Thr Arg Asn Met Thr Tyr Ser Ala Gly His Asn Leu Leu
270                               690                               695                               700
272 Lys Ala His Ala Leu Ala Trp His Val Tyr Asn Glu Lys Phe Arg His
273 705                               710                               715                               720
275 Ala Gln Asn Gly Lys Ile Ser Ile Ala Leu Gln Ala Asp Trp Ile Glu
276                               725                               730                               735
278 Pro Ala Cys Pro Phe Ser Gln Lys Asp Lys Glu Val Ala Glu Arg Val
279                               740                               745                               750
281 Leu Glu Phe Asp Ile Gly Trp Leu Ala Glu Pro Ile Phe Gly Ser Gly
282                               755                               760                               765
284 Asp Tyr Pro Trp Val Met Arg Asp Trp Leu Asn Gln Arg Asn Asn Phe
285                               770                               775                               780
287 Leu Leu Pro Tyr Phe Thr Glu Asp Glu Lys Lys Leu Ile Gln Gly Thr

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288 785          790          795          800
290 Phe Asp Phe Leu Ala Leu Ser His Tyr Thr Thr Ile Leu Val Asp Ser
291          805          810          815
293 Glu Lys Glu Asp Pro Ile Lys Tyr Asn Asp Tyr Leu Glu Val Gln Glu
294          820          825          830
296 Met Thr Asp Ile Thr Trp Leu Asn Ser Pro Ser Gln Val Ala Val Val
297          835          840          845
299 Pro Trp Gly Leu Arg Lys Val Leu Asn Trp Leu Lys Phe Lys Tyr Gly
300          850          855          860
302 Asp Leu Pro Met Tyr Ile Ile Ser Asn Gly Ile Asp Asp Gly Leu His
303 865          870          875          880
305 Ala Glu Asp Asp Gln Leu Arg Val Tyr Tyr Met Gln Asn Tyr Ile Asn
306          885          890          895
308 Glu Ala Leu Lys Ala His Ile Leu Asp Gly Ile Asn Leu Cys Gly Tyr
309          900          905          910
311 Phe Ala Tyr Ser Phe Asn Asp Arg Thr Ala Pro Arg Phe Gly Leu Tyr
312          915          920          925
314 Arg Tyr Ala Ala Asp Gln Phe Glu Pro Lys Ala Ser Met Lys His Tyr
315          930          935          940
317 Arg Lys Ile Ile Asp Ser Asn Gly Phe Pro Gly Pro Glu Thr Leu Glu
318 945          950          955          960
320 Arg Phe Cys Pro Glu Glu Phe Thr Val Cys Thr Glu Cys Ser Phe Phe
321          965          970          975
323 His Thr Arg Lys Ser Leu Leu Ala Phe Ile Ala Phe Leu Phe Phe Ala
324          980          985          990
326 Ser Ile Ile Ser Leu Ser Leu Ile Phe Tyr Tyr Ser Lys Lys Gly Arg
327          995          1000          1005
329 Arg Ser Tyr Lys
330 1010
334 <210> SEQ ID NO: 3
335 <211> LENGTH: 549
336 <212> TYPE: PRT
337 <213> ORGANISM: Homo sapiens
339 <400> SEQUENCE: 3
340 Met Pro Ala Ser Ala Pro Pro Arg Arg Pro Arg Pro Pro Pro Gln Ser
341 1 5 10 15
343 Leu Ser Leu Leu Leu Val Leu Leu Gly Leu Gly Gly Arg Arg Leu Arg
344 20 25 30
346 Ala Glu Pro Gly Asp Gly Ala Gln Thr Trp Ala Arg Phe Ser Arg Pro
347 35 40 45
349 Pro Ala Pro Glu Ala Ala Gly Leu Phe Gln Gly Thr Phe Pro Asp Gly
350 50 55 60
352 Phe Leu Trp Ala Val Gly Ser Ala Ala Tyr Gln Thr Glu Gly Gly Trp
353 65 70 75 80
355 Gln Gln His Gly Lys Gly Ala Ser Ile Trp Asp Thr Phe Thr His His
356 85 90 95
358 Pro Leu Ala Pro Pro Gly Asp Ser Arg Asn Ala Ser Leu Pro Leu Gly
359 100 105 110
361 Ala Pro Ser Pro Leu Gln Pro Ala Thr Gly Asp Val Ala Ser Asp Ser

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VERIFICATION SUMMARY

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